

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/579,622
Source: IFWP
Date Processed by STIC: 5/26/06

ENTERED



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/579,622

DATE: 05/26/2006

TIME: 08:14:03

Input Set : A:\Sequence Listing.txt
 Output Set: N:\CRF4\05262006\J579622.raw

5 <110> APPLICANT: Crusade Laboratories Limited
 7 Sloane-Kettering Institute for Cancer Research
 9 Brown, Susanne M
 11 Dunn, Paul
 13 Singh, Bhuvanesh
 15 Ganly, Ian
 19 <120> TITLE OF INVENTION: Mutant Viruses
 23 <130> FILE REFERENCE: 6947-75757-01
 C--> 27 <140> CURRENT APPLICATION NUMBER: US/10/579,622
 C--> 27 <141> CURRENT FILING DATE: 2006-05-16
 27 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/004908
 29 <151> PRIOR FILING DATE: 2004-11-17
 33 <150> PRIOR APPLICATION NUMBER: GB 0326798.6
 35 <151> PRIOR FILING DATE: 2003-11-17
 39 <150> PRIOR APPLICATION NUMBER: US 60/541,308
 41 <151> PRIOR FILING DATE: 2004-02-03
 45 <160> NUMBER OF SEQ ID NOS: 6
 49 <170> SOFTWARE: PatentIn version 3.1
 53 <210> SEQ ID NO: 1
 55 <211> LENGTH: 918
 57 <212> TYPE: DNA
 59 <213> ORGANISM: Homo sapiens
 63 <220> FEATURE:
 65 <221> NAME/KEY: CDS
 67 <222> LOCATION: (58)..(837)
 71 <400> SEQUENCE: 1
 72 cgcctgtccat tcgctgcgga gccggaggag gaggggagag gcctggagga caccaac 57
 74 atg aac aag ttg aaa tca tcg cag aag gat aaa gtt cgt cag ttt atg 105
 75 Met Asn Lys Leu Lys Ser Ser Gln Lys Asp Lys Val Arg Gln Phe Met
 76 1 5 10 15
 78 atc ttc aca caa tct agt gaa aaa aca gca gta agt tgt ctt tct caa 153
 79 Ile Phe Thr Gln Ser Ser Glu Lys Thr Ala Val Ser Cys Leu Ser Gln
 80 20 25 30
 82 aat gac tgg aag tta gat gtt gca aca gat aat ttt ttc caa aat cct 201
 83 Asn Asp Trp Lys Leu Asp Val Ala Thr Asp Asn Phe Phe Gln Asn Pro
 84 35 40 45
 86 gaa ctt tat ata cga gag agt gta aaa gga tca ttg gac agg aag aag 249
 87 Glu Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu Asp Arg Lys Lys
 88 50 55 60
 90 tta gaa cag ctg tac aat aga tac aaa gac cct caa gat gag aat aaa 297
 91 Leu Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln Asp Glu Asn Lys
 92 65 70 75 80
 94 att gga ata gat ggc ata cag cag ttc tgt gat gac ctg gca ctc gat 345

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96				85					90						95		
98	cca	gcc	agc	att	agt	gtg	ttg	att	att	gca	tgg	aag	ttc	aga	gca	gca	393
99	Pro	Ala	Ser	Ile	Ser	Val	Leu	Ile	Ile	Ala	Trp	Lys	Phe	Arg	Ala	Ala	
100				100					105						110		
102	aca	cag	tgc	gag	ttc	tcc	aaa	cag	gag	ttc	atg	gat	ggc	atg	aca	gaa	441
103	Thr	Gln	Cys	Glu	Phe	Ser	Lys	Gln	Glu	Phe	Met	Asp	Gly	Met	Thr	Glu	
104		115						120						125			
106	tta	gga	tgt	gac	agc	ata	gaa	aaa	cta	aag	gcc	cag	ata	ccc	aag	atg	489
107	Leu	Gly	Cys	Asp	Ser	Ile	Glu	Lys	Leu	Lys	Ala	Gln	Ile	Pro	Lys	Met	
108		130						135						140			
110	gaa	caa	gaa	ttg	aaa	gaa	cca	gga	cga	ttt	aag	gat	ttt	tac	cag	ttt	537
111	Glu	Gln	Glu	Leu	Lys	Glu	Pro	Gly	Arg	Phe	Lys	Asp	Phe	Tyr	Gln	Phe	
112	145				150					155					160		
114	act	ttt	aat	ttt	gca	aag	aat	cca	gga	caa	aaa	gga	tta	gat	ctt	gaa	585
115	Thr	Phe	Asn	Phe	Ala	Lys	Asn	Pro	Gly	Gln	Lys	Gly	Leu	Asp	Leu	Glu	
116		165					170						175				
118	atg	gcc	att	gcc	tac	tgg	aac	tta	gtg	ttt	aat	gga	aga	ttt	aaa	ttc	633
119	Met	Ala	Ile	Ala	Tyr	Trp	Asn	Leu	Leu	Asn	Gly	Arg	Phe	Lys	Phe		
120		180					185						190				
122	tta	gac	tta	tgg	aat	aaa	ttt	ttg	ttg	gaa	cat	cat	aaa	cga	tca	ata	681
123	Leu	Asp	Leu	Trp	Asn	Lys	Phe	Leu	Leu	Glu	His	His	Lys	Arg	Ser	Ile	
124		195					200						205				
126	cca	aaa	gac	act	tgg	aat	ctt	ctt	tta	gac	ttc	agt	acg	atg	att	gca	729
127	Pro	Lys	Asp	Thr	Trp	Asn	Leu	Leu	Asp	Phe	Ser	Thr	Met	Ile	Ala		
128		210					215						220				
130	gat	gac	atg	tct	aat	tat	gat	gaa	gaa	gca	tgg	cct	gtt	ctt	att		777
131	Asp	Asp	Met	Ser	Asn	Tyr	Asp	Glu	Glu	Gly	Ala	Trp	Pro	Val	Leu	Ile	
132	225				230				235					240			
134	gat	gac	ttt	gtg	gaa	ttt	gca	cgc	cct	caa	att	gct	ggg	aca	aaa	agt	825
135	Asp	Asp	Phe	Val	Glu	Phe	Ala	Arg	Pro	Gln	Ile	Ala	Gly	Thr	Lys	Ser	
136		245					250						255				
138	aca	aca	gtg	tag	cactaaagga	accttctaga	atgtacatag	tctgtacaat									877
139	Thr	Thr	Val														
142	aaataacaaca	gaaaattgca	cagtcaattt	ctgctggctg	g												918
145	<210>	SEQ ID NO:	2														
147	<211>	LENGTH:	259														
149	<212>	TYPE:	PRT														
151	<213>	ORGANISM:	Homo sapiens														
155	<400>	SEQUENCE:	2														
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158	1			5				10						15			
161	Ile	Phe	Thr	Gln	Ser	Ser	Glu	Lys	Thr	Ala	Val	Ser	Cys	Leu	Ser	Gln	
162		20					25						30				
165	Asn	Asp	Trp	Lys	Leu	Asp	Val	Ala	Thr	Asp	Asn	Phe	Phe	Gln	Asn	Pro	
166		35					40						45				
169	Glu	Leu	Tyr	Ile	Arg	Glu	Ser	Val	Lys	Gly	Ser	Leu	Asp	Arg	Lys	Lys	
170		50					55						60				
173	Leu	Glu	Gln	Leu	Tyr	Asn	Arg	Tyr	Lys	Asp	Pro	Gln	Asp	Glu	Asn	Lys	

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174	65	70	75	80	
177	Ile Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp Leu Ala Leu Asp				
178		85	90	95	
181	Pro Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys Phe Arg Ala Ala				
182		100	105	110	
185	Thr Gln Cys Glu Phe Ser Lys Gln Glu Phe Met Asp Gly Met Thr Glu				
186		115	120	125	
189	Leu Gly Cys Asp Ser Ile Glu Lys Leu Lys Ala Gln Ile Pro Lys Met				
190		130	135	140	
193	Glu Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp Phe Tyr Gln Phe				
194		145	150	160	
197	Thr Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly Leu Asp Leu Glu				
198		165	170	175	
201	Met Ala Ile Ala Tyr Trp Asn Leu Val Leu Asn Gly Arg Phe Lys Phe				
202		180	185	190	
205	Leu Asp Leu Trp Asn Lys Phe Leu Leu Glu His His Lys Arg Ser Ile				
206		195	200	205	
209	Pro Lys Asp Thr Trp Asn Leu Leu Leu Asp Phe Ser Thr Met Ile Ala				
210		210	215	220	
213	Asp Asp Met Ser Asn Tyr Asp Glu Glu Gly Ala Trp Pro Val Leu Ile				
214		225	230	235	240
217	Asp Asp Phe Val Glu Phe Ala Arg Pro Gln Ile Ala Gly Thr Lys Ser				
218		245	250	255	
221	Thr Thr Val				
225	<210> SEQ ID NO: 3				
227	<211> LENGTH: 876				
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237	<221> NAME/KEY: CDS				
239	<222> LOCATION: (16)..(795)				
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245		Met Asn Lys Leu Lys Ser Ser Gln Lys Asp Lys Val			
246		1	5	10	
248	cgt cag ttt atg atc ttc aca caa tct agt gaa aaa aca gca gta agt				
249	Arg Gln Phe Met Ile Phe Thr Gln Ser Ser Glu Lys Thr Ala Val Ser				
250		15	20	25	
252	tgt ctt tct caa aat gac tgg aag tta gat gtt gca aca gat aat ttt			147	
253	Cys Leu Ser Gln Asn Asp Trp Lys Leu Asp Val Ala Thr Asp Asn Phe				
254		30	35	40	
256	tcc caa aat cct gaa ctt tat ata cga gag agt gta aaa gga tca ttg			195	
257	Phe Gln Asn Pro Glu Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu				
258		45	50	55	60
260	gac agg aag aag tta gaa cag ctg tac aat aga tac aaa gac cct caa				
261	Asp Arg Lys Lys Leu Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln				
262		65	70	75	
264	gat gag aat aaa att gga ata gat ggc ata cag cag ttc tgt gat gac				
265	Asp Glu Asn Lys Ile Gly Ile Asp Gly Ile Gln Gln Phe Cys Asp Asp				
266		291			

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Input Set : A:\Sequence Listing.txt
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266	80	85	90	
268	ctg gca ctc gat cca gcc agc att agt gtg ttg att att	gcg tgg aag		339
269	Leu Ala Leu Asp Pro Ala Ser Ile Ser Val Leu Ile Ile Ala Trp Lys			
270	95	100	105	
272	tgc aga gca gca aca cag tgc gag ttc tcc aaa cag gag ttc atg gat			387
273	Phe Arg Ala Ala Thr Gln Cys Glu Phe Ser Lys Gln Glu Phe Met Asp			
274	110	115	120	
276	ggc atg aca gaa tta gga tgt gac agc aca gaa aaa cta aag gcc cag			435
277	Gly Met Thr Glu Leu Gly Cys Asp Ser Thr Glu Lys Leu Lys Ala Gln			
278	125	130	135	140
280	ata ccc aag atg gaa caa gaa ttg aaa gaa cca gga cga ttt aag gat			483
281	Ile Pro Lys Met Glu Gln Glu Leu Lys Glu Pro Gly Arg Phe Lys Asp			
282	145	150	155	
284	ttt tac cag ttt act ttt aat ttt gca aag aat cca gga caa aaa gga			531
285	Phe Tyr Gln Phe Thr Phe Asn Phe Ala Lys Asn Pro Gly Gln Lys Gly			
286	160	165	170	
288	tta gat cta gaa atg gcc att gcc tac tgg aac tta gtg ctt aat gga			579
289	Leu Asp Leu Glu Met Ala Ile Ala Tyr Trp Asn Leu Val Leu Asn Gly			
290	175	180	185	
292	aga ttt aga ctc tta gac tta tgg aat aaa ttt ttg ttg gaa cat cat			627
293	Arg Phe Arg Leu Leu Asp Leu Trp Asn Lys Phe Leu Leu Glu His His			
294	190	195	200	
296	aaa cga tca ata cca aaa gac act tgg aat ctt ctt tta gac ttc agt			675
297	Lys Arg Ser Ile Pro Lys Asp Thr Trp Asn Leu Leu Asp Phe Ser			
298	205	210	215	220
300	acg atg att gca gat gac atg tct aat tat gat gaa gaa gga gca tgg			723
301	Thr Met Ile Ala Asp Asp Met Ser Asn Tyr Asp Glu Glu Gly Ala Trp			
302	225	230	235	
304	cct gtt ctt att gat gac ttt gtg gaa ttt gca cgc cct caa att gct			771
305	Pro Val Leu Ile Asp Asp Phe Val Glu Phe Ala Arg Pro Gln Ile Ala			
306	240	245	250	
308	ggg aca aaa agt aca aca gtg tag cactaaagga accttctaga atgtacatag			825
309	Gly Thr Lys Ser Thr Thr Val			
310	255			
312	tctgtacaat aaatacaaca gaaaattgca cagtcaattt ctgctggctg g			876
315	<210> SEQ ID NO: 4			
317	<211> LENGTH: 259			
319	<212> TYPE: PRT			
321	<213> ORGANISM: Homo sapiens			
325	<400> SEQUENCE: 4			
327	Met Asn Lys Leu Lys Ser Ser Gln Lys Asp Lys Val Arg Gln Phe Met			
328	1	5	10	15
331	Ile Phe Thr Gln Ser Ser Glu Lys Thr Ala Val Ser Cys Leu Ser Gln			
332	20	25	30	
335	Asn Asp Trp Lys Leu Asp Val Ala Thr Asp Asn Phe Phe Gln Asn Pro			
336	35	40	45	
339	Glu Leu Tyr Ile Arg Glu Ser Val Lys Gly Ser Leu Asp Arg Lys Lys			
340	50	55	60	
343	Leu Glu Gln Leu Tyr Asn Arg Tyr Lys Asp Pro Gln Asp Glu Asn Lys			

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344	65	70	75	80												
347	Ile	Gly	Ile	Asp	Gly	Ile	Gln	Gln	Phe	Cys	Asp	Asp	Leu	Ala	Leu	Asp
348						85				90					95	
351	Pro	Ala	Ser	Ile	Ser	Val	Leu	Ile	Ile	Ala	Trp	Lys	Phe	Arg	Ala	Ala
352						100				105					110	
355	Thr	Gln	Cys	Glu	Phe	Ser	Lys	Gln	Glu	Phe	Met	Asp	Gly	Met	Thr	Glu
356						115				120					125	
359	Leu	Gly	Cys	Asp	Ser	Thr	Glu	Lys	Leu	Lys	Ala	Gln	Ile	Pro	Lys	Met
360						130				135					140	
363	Glu	Gln	Glu	Leu	Lys	Glu	Pro	Gly	Arg	Phe	Lys	Asp	Phe	Tyr	Gln	Phe
364						145				150					155	
367	Thr	Phe	Asn	Phe	Ala	Lys	Asn	Pro	Gly	Gln	Lys	Gly	Leu	Asp	Leu	Glu
368						165				170					175	
371	Met	Ala	Ile	Ala	Tyr	Trp	Asn	Leu	Val	Leu	Asn	Gly	Arg	Phe	Arg	Leu
372						180				185					190	
375	Leu	Asp	Leu	Trp	Asn	Lys	Phe	Leu	Leu	Glu	His	His	Lys	Arg	Ser	Ile
376						195				200					205	
379	Pro	Lys	Asp	Thr	Trp	Asn	Leu	Leu	Leu	Asp	Phe	Ser	Thr	Met	Ile	Ala
380						210				215					220	
383	Asp	Asp	Met	Ser	Asn	Tyr	Asp	Glu	Glu	Gly	Ala	Trp	Pro	Val	Leu	Ile
384						225				230					235	
387	Asp	Asp	Phe	Val	Glu	Phe	Ala	Arg	Pro	Gln	Ile	Ala	Gly	Thr	Lys	Ser
388						245				250					255	
391	Thr	Thr	Val													
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397	<211>	LENGTH:	64													
399	<212>	TYPE:	DNA													
401	<213>	ORGANISM:	Artificial sequence													
405	<220>	FEATURE:														
407	<223>	OTHER INFORMATION:	DNA nucleotide sequence encoding the siRNA construct designed to													
408		target expression of the SCCRO gene														
410	<400>	SEQUENCE:	5													
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413	gaaa														64	
416	<210>	SEQ ID NO:	6													
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420	<212>	TYPE:	DNA													
422	<213>	ORGANISM:	Artificial sequence													
426	<220>	FEATURE:														
428	<223>	OTHER INFORMATION:	Nucleotide sequence encoding control siRNA													
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431	gatccccgtt	ctacctacac	tccctttca	agagagagg	agtgttaggt	gacgtttta									60	

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/579,622

DATE: 05/26/2006
TIME: 08:14:04

Input Set : A:\Sequence Listing.txt
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L:27 M:271 C: Current Filing Date differs, Replaced Current Filing Date